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A New *Paracymoriza* Species from Lombok (Indonesia) (Lepidoptera, Crambidae)¹

Wolfgang SPEIDEL¹⁾, Ulf BUCHSBAUM²⁾ & Michael A. MILLER²⁾

¹⁾Zoologisches Forschungsmuseum Alexander Koenig, Bonn (Germany)

²⁾Zoologische Staatssammlung, Munich (Germany)

Abstract. A new species *Paracymoriza naumanniella* sp. nov. from Lombok island is described and assigned to the *Paracymoriza albifascialis* species group. Moreover, data on the egg structure, habitat, and behaviour of the adult moths are given. In addition, DNA sequence information of mitochondrial cytochrome oxidase subunit I are furnished, which constitute the first report of genetic data concerning this gene within the family Crambidae.

Key words: Acentropinae, *Paracymoriza naumanniella* sp. nov., taxonomy, mtDNA, COI

1. INTRODUCTION

The genus *Paracymoriza* Warren, 1890 is a species rich genus within the family Crambidae, belonging to the superfamily Pyraloidea (Pyralid moths). Within the Crambidae, it is a member of the subfamily Acentropinae (former Nymphulinae, aquatic moths). In the past, *Paracymoriza* has been treated as a synonym of *Parthenodes* Guenée, 1854 which is an unrelated genus which has, in contrast, an exclusively new world distribution. *Paracymoriza* comprises 28 currently recognized species in the Oriental Region (SPEIDEL & MEY 1999; SPEIDEL 2003). The new species occurs in Lombok, Indonesia and seems to be closely associated with humid ecosystems where the specimens of the type series have been found.

2. TAXONOMY

Paracymoriza naumanniella sp. nov. (Figs. 1 A, 1 B, 2 a, 2 b)

Material: Holotype ♂: “Indonesia, North Lombok, Gunung Rinjani NP, Air terjun, near village Senaru, ca. 500 - 600 m, 08°18' S / 116°24' E, 28. Dezember 2003, TF, leg. Mei-Yu Chen & Ulf Buchsbaum”. “DNATAX 02820”; genitalia slide no.: M3450 Zoologische Staatssammlung München (Munich, Germany).

11 paratypes: same data, one ♀ with genitalia slide no. M3451 in Zoologische Staatssammlung München, 2 paratypes in Museum für Naturkunde, Berlin (one of them with additional label “DNATAX02824”) and 2 paratypes in coll. W. Speidel, Bonn (one with additional label “DNATAX02822”).

DNA is stored in the frozen DNA collection of the ZSM under storage numbers DNATAX02820 (holotype), DNATAX02821 (paratype), DNATAX02822 (paratype), DNATAX02823 (paratype), DNATAX02824 (paratype), and DNATAX02825 (paratype).

Description: Length of forewing: ♂ 9 – 11mm, ø 10 mm; ♀ 9 – 11 mm, ø 10,2 mm.

Wingspan: ♂ 17 – 22 mm, ø 17,8 mm; ♀ 19 – 23 mm, ø 21 mm.

Body dark grey, abdomen with white intersegmental rings. White ground-colour of the wings strongly reduced, therefore pattern not very contrasting.

Forewing: Inner, medial and submarginal areas dark grey, basal area almost black. Basal, proximal and distal fascia narrow, whitish. Distal fascia strongly incurved close to inner termen, with a dent directed towards the termen on vein CuP. Some marginal white spots along the termen, fringe blackish.

Hindwing: In contrast to other small *Paracymoriza* species, the wing pattern is clearly visible, though the medial area is strongly suffused like in the forewing. Basal, proximal and distal fascia narrow, whitish. The distal fascia with outwardly directed dent. Discal spot black, very close to proximal fascia.

♂ **genitalia** (Fig. 3): Valva distally rounded, elongate, reminiscent of the other members in the genus, however only with two large, acute inwardly directed, apical, setae and several smaller hairs along the distal margin. Uncus elongate, rounded towards end, gnathos slender with very inconspicuous teeth. Aedeagus comparatively strong, without cornuti, bulbus ejaculatorius arising from this center.

¹ In commemoration of Clas Michael Naumann zu Königsbrück (26.06.1939 – 15.02.2004)



Fig. 1: *Paracymoriza naumanniella* sp. n. Holotype (male) (A) and one Paratype (female) (B). Indonesia, North Lombok, Gunung Rinjani NP, Air terjun, near village Senaru, ca. 500 - 600 m, 08°18' S / 116°24' E, 28. Dezember 2003, TF, leg. Mei-Yu Chen & Ulf Buchsbaum.



Fig. 2a-b: Paratypes of the new species still alive at the type locality in Lombok (see above). Photo: Ulf Buchsbaum.

♀ *genitalia* (Fig. 4): Ovipositor short, with long, slender, fragile apophyses. Ductus bursae rather long, gradually widening towards corpus bursae, with an unusual evagination about in its middle. Corpus bursae round, ball-shaped, without a clear signum. Colliculum situated terminally, with the slender ductus seminalis originating inside and in a short distance of the colliculum. Ostial region strongly sclerotized, large, cup-shaped, narrowing strongly towards the ductus bursae.

Egg (Fig. 7a, b): Oval, with micropylar zone at the narrow end of the egg (size: 310 x 180 µm).

Distribution (maps, Figs. 5a and 5b): Hitherto only known from the type locality in Lombok.

Genetic data: We sequenced the mitochondrial gene cytochrome oxidase subunit I in order to provide a molecular dataset for subsequent re-identification of the new species as recommended by TAUTZ et al. (2003). This gene has proven its usefulness for DNA taxonomy purposes in many studies (e.g. HEBERT et al. 2003).

Genetic characterization: Method: DNA was extracted from abdominal tissue of some of the type specimens of *P. naumanniella* sp. nov. using Qiagen (Hilden, Germany) tissue kit according to the protocol of KNÖLKE et al. (2005). Mitochondrial (mtDNA) cytochrome oxidase subunit I (COI) gene was amplified with PCR using protocols and primers as in SIMON et al. (1994). Direct sequencing of dye labelled templates was carried

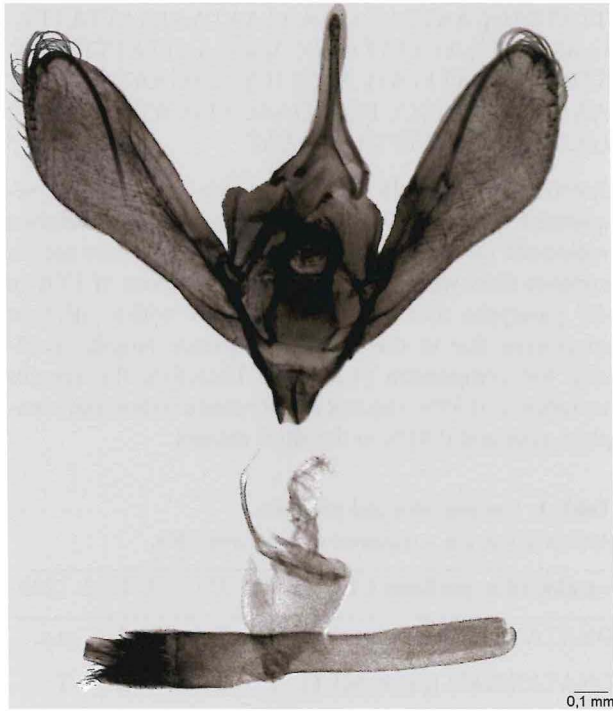


Fig. 3: Holotype male genitalia.

out using an ABI 377 automated sequencer (Applied Biosystems). Up to 10 single sequences per individual were assembled and aligned to the COI gene of *Bombyx mori* (L., 1758) (Lepidoptera, Bombycidae; GenBank accession number NC_002355).

Result: The following sequence of *P. naumanniella* sp. nov. shows the partial COI gene of the holotype:

>Paracymoriza_naumanniella_Holotype_
DNATAX02820_1230bp

CGAAAATGACTTTATTCTACAAATCATAAAGAT
ATTGGAACCTTTATATTTTATTTTGGAAATTTGAT
CGGGAATAGTTGGAACATCTTTAAGATTATTA
TTTCGAGCTGAATTAGGAAATCCTGGATCATTA
TTGGAGATGATCAAATTTATAATACTATTGT
CTGCTCATGCTTTTATTATAATTTTTTTTATAGT
AATGCCAATTATAATTGGAGGATTTGGAAATTG
ATTAGTTCCATTAATATTAGGTGCTCCTGATAT
GGCTTTCCACGAATAAATAATATAAGATTTTG
ACTTCTCCTCCATCTCTTACACTTTTAATTTCA
AGAAGAATCGTAGAAAATGGAGCAGGAACAGG
ATGAACAGTGTACCCCCACTATCATCTAATAT
CGCTCATGGAGGAAGATCTGTAGATTTAGCTAT
TTTTTCCTTACATTTAGCTGGTATTTCTCAATT
TTAGGAGCAATTAATTTCACTACTACAATTATT
AACATACGAATTAATAATTTATTTTTTGATCAA
ATACCTCTTTTTATTTGAGCGGTAGGTATTACA
GCTTTACTTCTTCTTCTTTCTTTACCAGTTTTAGC
TGGAGCAATTACTATGTTATTAACAGATCGAAA
TTTAAATACATCTTTTTTTTGATCCTGCTGGAGGA

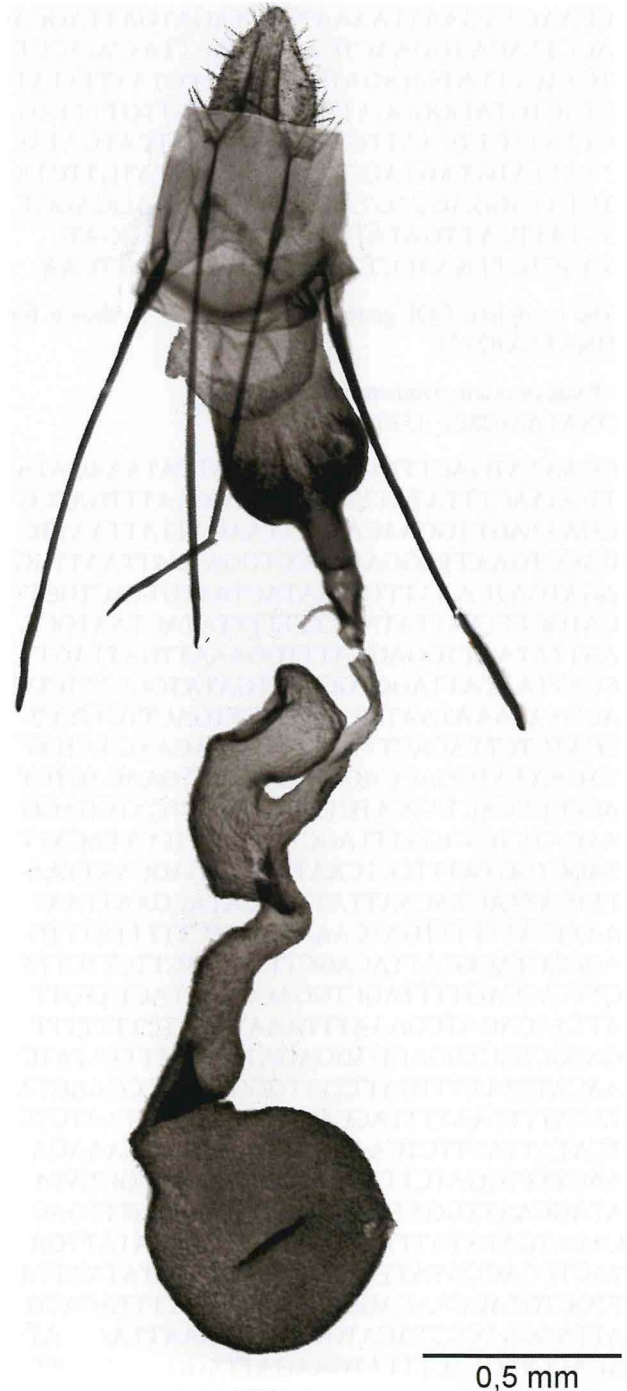


Fig. 4: Paratype female genitalia.

GGAGATCCAATTTTATATCAACATTTATTTTGGAT
TTTTTGGGCATCCCGAAGTATATATTTTAATTTT
ACCAGGATTTGGAATAATCTCTCATATTATTTCT
CAAGAAAGAGGAAAAAAGAACTTTTGGATC
TTTAGGAATAATTTATGCTATAATAGCAATTGG
ATTATTAGGATTTGTTGTTTGGACACATCATAT
ATTTACTGTAGGTATAGATATTGATACTCGAGC
ATATTTTACTTCTGCAACTATAATTATTGCTGTA

CCAACAGGAATTAAAATTTTATAGATGATTAGCA
ACCTTACATGGAACCTCAAATTAATTATAGACCT
TCTACTTTATGAAGATTAGGATTTGTATTTTAT
TTACTGTAGGGGGATTAAGTGGAGTTGTTTTAG
CTAATTCTTCAATTGATGTAGCTCTTCATGATAC
TTATTATGTAGTAGCACATTTTCATTATGTTCTA
TCTATAGGAGCAGTATTTGCTATTTTAGGAGGT
TTTATTCATTGATATCCATTATTTACAGGAT-
TAAGTCTTAAACCTTATTACTTAAAAATTCAA

The complete COI gene of the paratypes is shown for DNATAX02821:

>Paracymoriza_naumanniella_Paratype_
DNATAX02821_1530bp

CGAAAATGACTTTATTCTACAAATCATAAAGATA
TTGGAACTTTATATTTTATTTTGGAAATTTGATCG
GGAATAGTTGGAACATCTTTAAGATTATTAATTC
GAGCTGAATTAGGAAATCCTGGATCATTAAATTG
AGATGATCAAATTTATAATACTATTGTTACTGCT
CATGCTTTTATTATAATTTTTTTTATAGTAATGCC
AATTATAATTGGAGGATTTGGAAATTGATTAGTT
CCATTAATATTAGGTGCTCCTGATATGGCTTTCCC
ACGAATAAATAATATAAGATTTTGACTTCTTCCT
CCATCTCTTACACTTTTAATTTCAAGAAGAATCG
TAGAAAATGGAGCAGGAACAGGATGAACAGTGT
ACCCCCACTATCATCTAATATCGCTCATGGAGG
AAGATCTGTAGATTTAGCTATTTTTTCCTTACATT
TAGCTGGTATTTCTCAATTTTAGGAGCAATTAA
TTTCATTACTACAATTATTAACATACGAATTAAT
AATTTATTTTTGATCAAATACCTCTTTTTATTTG
AGCGGTAGGTATTACAGCTTTACTTCTTCTTTT
CTTTACCAGTTTTAGCTGGAGCAATTACTATGTT
ATTAACAGATCGAAATTTAAATACATCTTTTTTT
GATCCTGCTGGAGGAGGAGATCCAATTTTATATC
AACATTTATTTTGATTTTTTTGGGCATCCCGAAGTA
TATATTTTAATTTTACCAGGATTTGGAATAATCTC
TCATATTATTTCTCAAGAAAGAGGAAAAAAGA
AACTTTTGGATCTTTAGGAATAATTTATGCTATA
ATAGCAATTGGATTATTAGGATTTGTTGTTTGGAG
CACATCATATATTTACTGTAGGTATAGATATTGA
TACTCGAGCATATTTTACTTCTGCAACTATAATTA
TTGCTGTACCAACAGGAATTTAAATTTTTTAGATG
ATTAGCAACCTTACATGGAACCTCAAATTAATTAT
AGACCTTCTACTTTATGAAGATTAGGATTTGTAT
TTTTATTTACTGTAGGGGGATTAAGTGGAGTTGT
TTTAGCTAATTTCTCAATTGATGTAGCTCTTCATG
ATACTTATTATGTAGTAGCACATTTTCATTATGTT
CTATCTATAGGAGCAGTATTTGCTATTTTAGGAG
GTTTTATTCATTGATATCCATTATTTACAGGATTA
ACTCTTAAACCTTATTACTTAAAAATTCAATTTAT
TACAATATTTATTGGAGTAAATTTAACTTTTTTCC
CACAACATTTTTTAGGTTTAGCTGGAATACCACG
ACGATATTCTGATTATCCTGACATTTATATTTTCAT
GAAATATTATTTCTTCATTAGGATCTTATATTTCA

TTATTAGCAATTATAATAATAATAATAATTATTT
GAGAATCAATAATTAACCAACGAATTATTTTATT
TTCATTAAATTTATCATCTTCTATTGAATGATATC
AAAATTTACCCCCTGCAGAACATTCATATAAT-
GAACTTCCTATTTTAAGAAAT

Species variation: In addition to the holotype we sequenced four of the paratypes. The sequence variation within the set of types is shown in Table 1. There are six variable sites within the complete sequences of COI of the paratypes and five variable sites within all type specimens due to the reduced sequence lengths available for comparison (1,230bp). Therefore the species variation is 0.39% sequence divergence within the complete gene and 0.41% in the short dataset.

Table 1: Variable sites and positions.

Abbreviation: n.a. - sequence data not available.

| variable sites: | positions | COI | 69 | 309 | 351 | 708 | 1113 | 1283 |
|------------------------|-----------|-----|----|-----|-----|------|------|------|
| DNATAX02820 (holotype) | G | T | T | G | A | n.a. | | |
| DNATAX02821 (paratype) | G | T | T | G | A | T | | |
| DNATAX02823 (paratype) | G | T | T | G | A | G | | |
| DNATAX02824 (paratype) | A | C | C | A | G | T | | |
| DNATAX02825 (paratype) | G | T | T | G | A | T | | |

The new sequences are deposited under the accession numbers AJ 852519 (DNATAX02820, holotype), AJ 852520 (DNATAX02821, paratype), AJ 852521 (DNATAX02823, paratype), AJ 852522 (DNATAX02824, paratype), and AJ 852523 (DNATAX02825, paratype), respectively, at EBI/GenBank.

Remarks on the molecular studies. The aim is to provide an additional character set in the diagnosis of the new species. There is at the moment no possibility to include related species in a differential diagnosis on DNA sequence level due to the missing COI data of other species of the family Crambidae.

Biological data: The imagines of the new species are so far found only in December. The biotope is a primary rain forest, near a waterfall, with very high humidity due to the mist.

The moths rest on the algae covered sides of stones and rocks situated close to or in the water. Eventually they jump onto the surface of the water and afterwards back to the rock. The moth are highly hydrophobic, can be completely submerged under waves, but are not trapped by the surface-tension of the water. They seem to be very connected to their restricted habitat and to leave it very rarely and only within little distances.

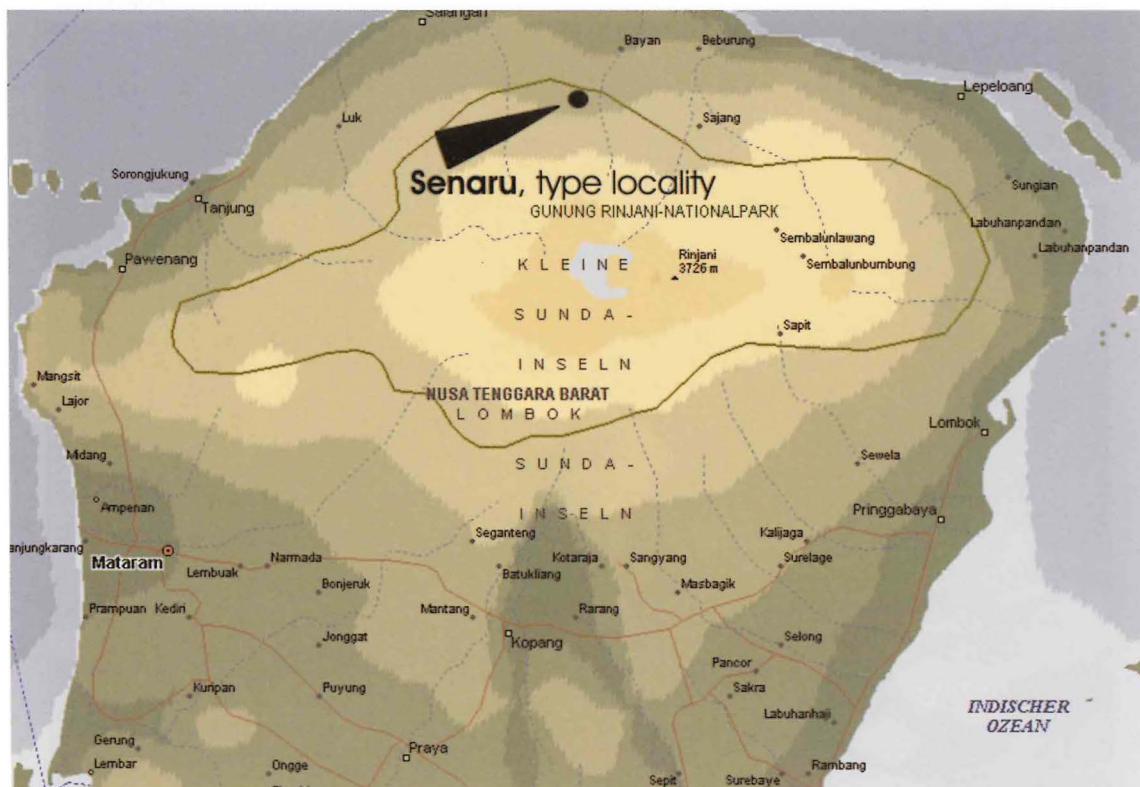
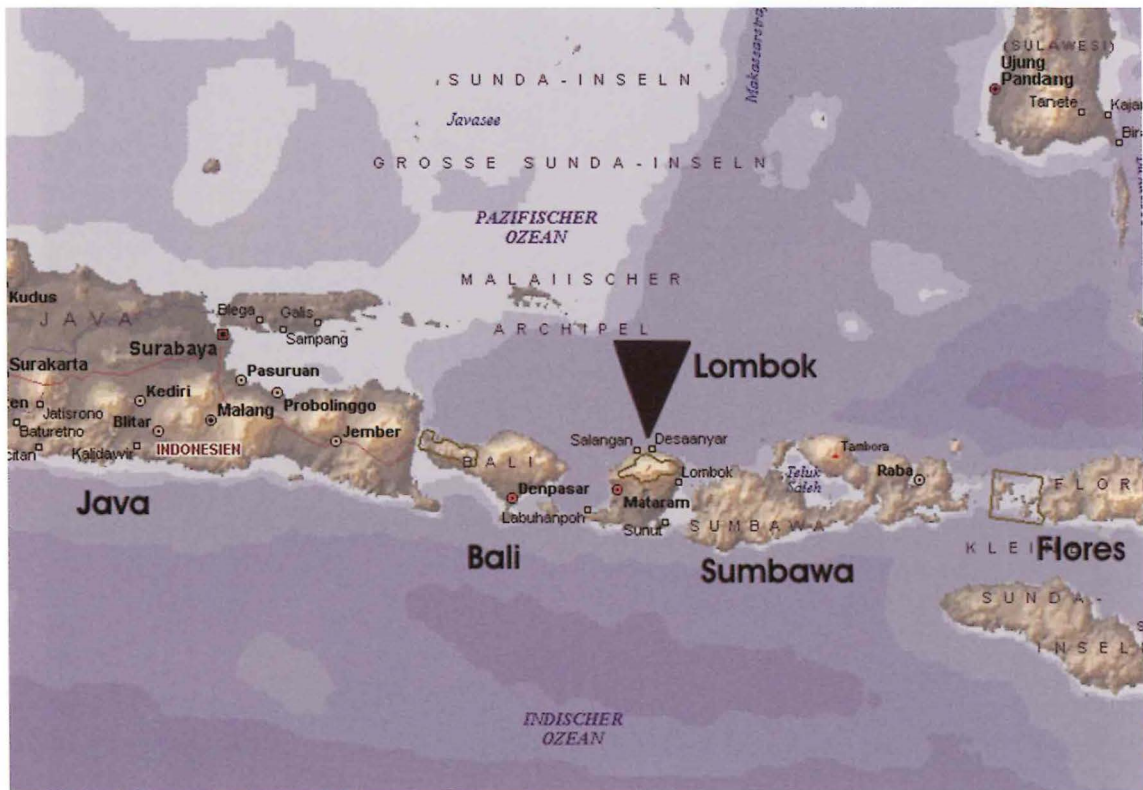


Fig 5: Type locality. 5 a: Enlarged view to show the situation of the Island Lombok (Indonesia) east of Bali; 5 b: type locality of *P. naumannella* on Lombok Island near the village Senaru below the mountain Gunung Rinjani.

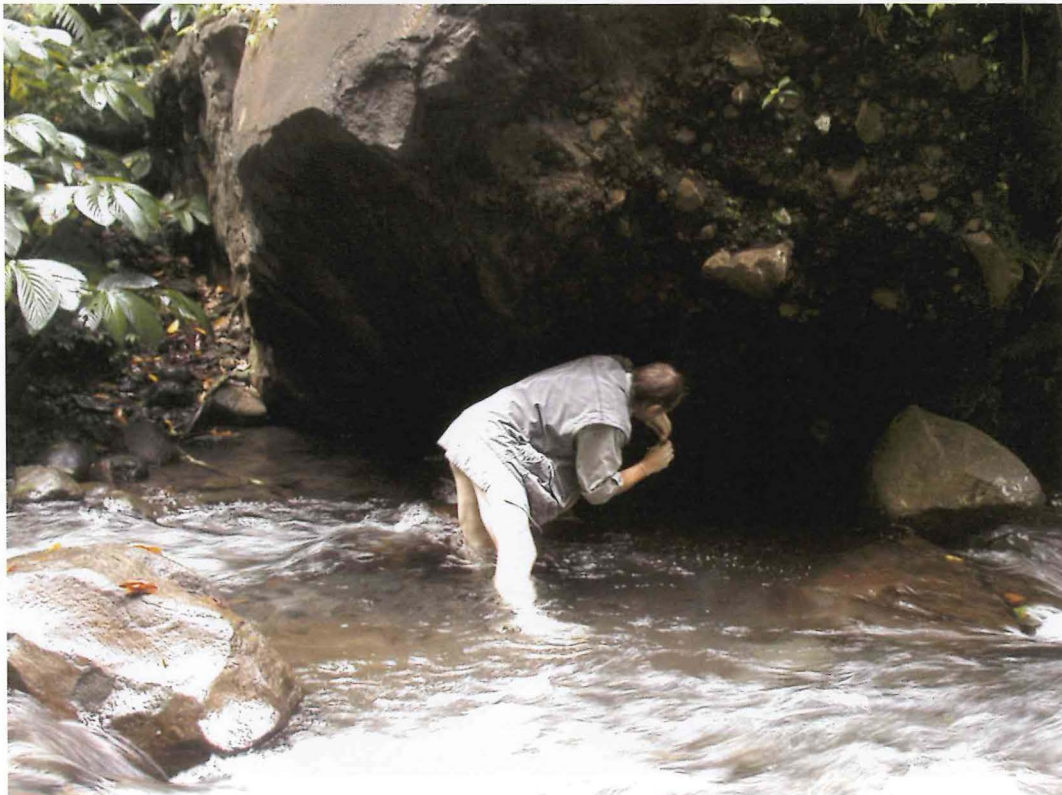


Fig. 6: Biotope at type locality beside the waterfall. 6 a: Here, most moths rest under the rocks near the water surface. Photo: Ulf Buchsbaum; 6 b: One of the authors (U. B.) collecting specimens of the new species. Photo: Mei-Yu Chen.

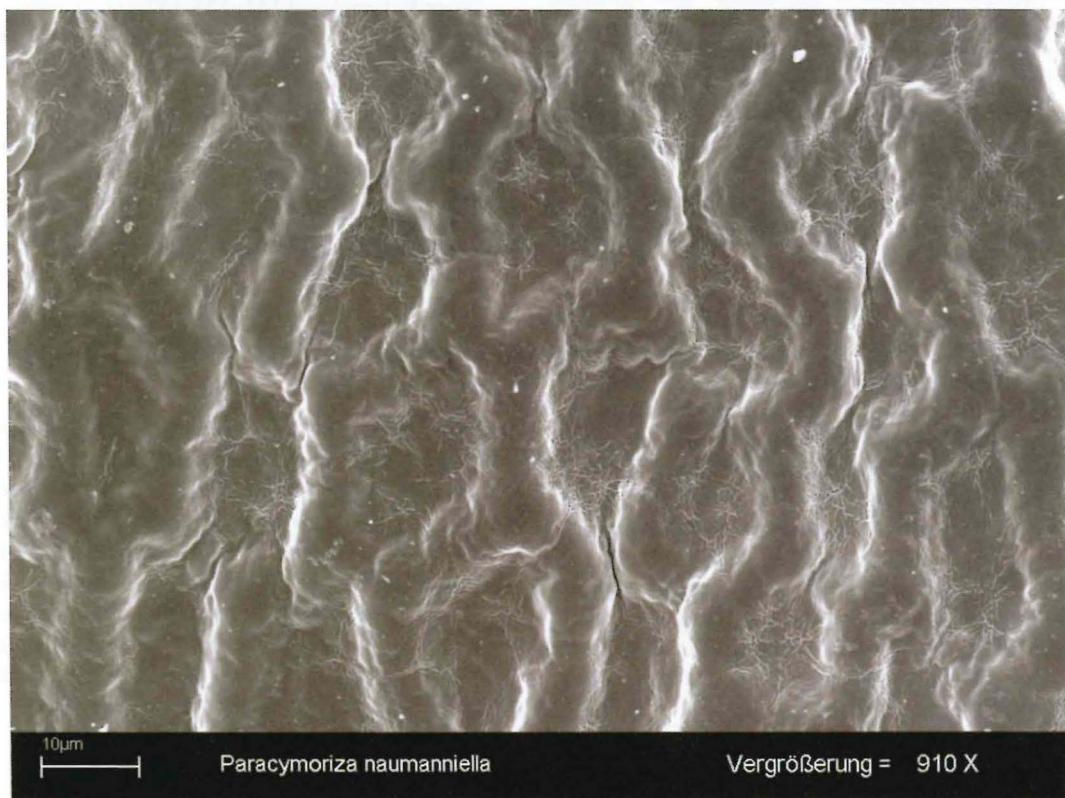
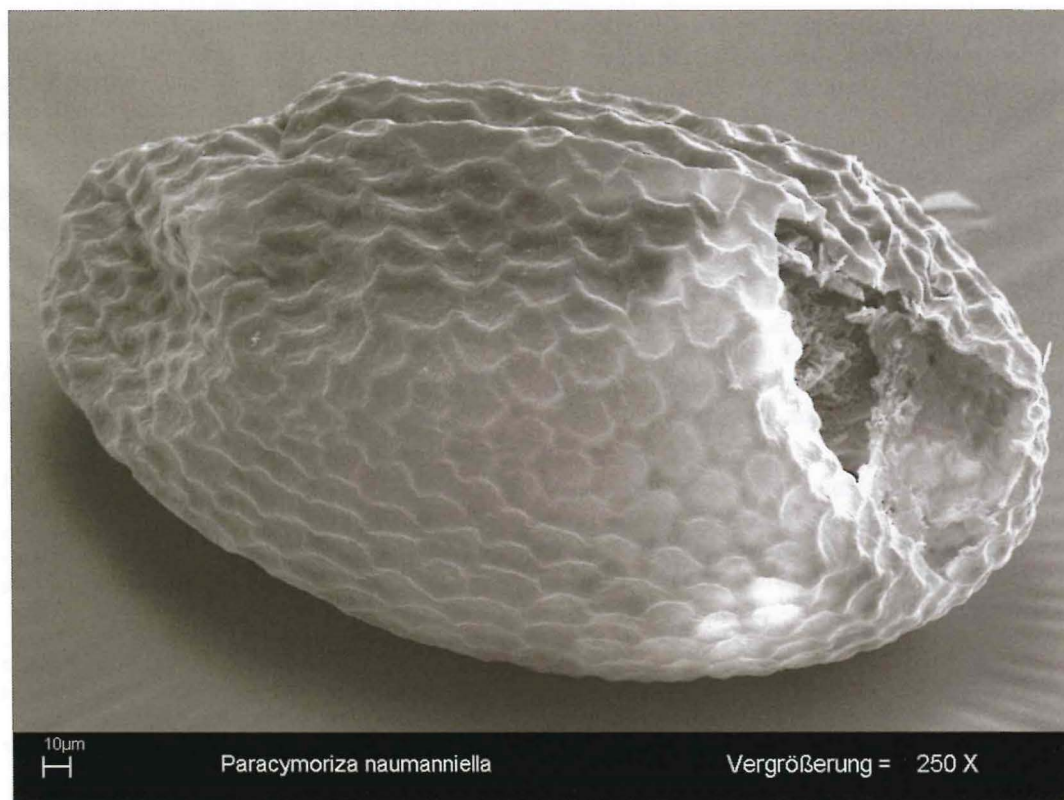


Fig. 7: SEM photos of the egg of *Paracymoriza naumanniella*. 7 a: Egg (total view); 7 b: surface structure of the egg with larger magnification.

Relationships: The closest relatives of the new species can only be ascertained after a revision of the genus. A similar wing-pattern is found in the *P. albifascialis* Hampson, 1891 species group (SPEIDEL & MEY 1999), especially in the strongly toothed distal fascia. It is therefore tentatively placed in this species group, but differs from all other members of the group by the infuscated medial area of both wing-pairs and the small size. Differences from the *Paracymoriza distinctalis* (Leech, 1889) group include the slender wing-shape (broader in the *P. distinctalis* species group) and the size (larger in the *P. distinctalis* species group). Members of the *P. nigra* (Warren, 1896) species group show the same small size, however the pattern is almost absent from the hindwing.

Etymology: The species is named in honour of the late Prof. Dr Clas M. NAUMANN, one of the most important contemporary lepidopterists who has successfully introduced and used the methods of Phylogenetic Systematics in lepidopterology.

3. DISCUSSION

The approach to include genetic data in new species descriptions is facing more and more acceptance within the scientific community. Proponents of the so-called 'DNA taxonomy' plea for the use of genetic markers as a unique determination tool (TAUTZ et al. 2003). The question which gene to use is tending to the well investigated COI gene of the mitochondrion (HEBERT et al. 2003). Critics of the choice refer to the risk of misleading results due to the analysis of paralogous sequences because of independent evolving nuclear insertions of mitochondrial genes (THALMANN et al. 2004). Nevertheless these rare exceptions should not keep taxonomists from producing genetic markers of newly described species. There is a major chance in the offering of genetic markers: Unknown immature stages can easily be associated with adult descriptions. Breeding of aquatic moths in the field is rather difficult and in the present case the early stages of *P. naumanniella* sp. nov. are unknown. The genetic data will enable to associate larvae in the future. The new species may have aquatic larvae, which probably live in the current water of small creeks close to the locations where the imagines were found. The assignment of unknown larvae to the species they belong, is only possible by analysis of their genome when rearing of the caterpillars is not feasible. Prof. Dr. Clas M. NAUMANN had been aware of the chances genetic markers offer for taxonomy. In his late years he hardly hesitated to become a proponent of DNA taxonomy, and his main focus still laid on the phylogenetic aspect which genetic information of taxa provides.

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Authors' addresses: Dr Wolfgang SPEIDEL (corresponding author), Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, D-53113 Bonn, Germany; e-mail: w.speidel.zfmk@uni-bonn.de; Ulf BUCHSBAUM, Zoologische Staatssammlung München, Münchhausenstraße 21, D-81247 München, Germany; e-mail: UlfBuchsbaum.Lepidoptera@zsm.mwn.de; Michael A. MILLER, Zoologische Staatssammlung München, Münchhausenstraße 21, D-81247 München, Germany; e-mail: miller@zsm.mwn.de

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